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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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10/590,705

06/14/2007

Shin-ichi Hashimoto

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EXAMINER

MEAH, MOHAMMAD Y

ART UNIT

PAPER NUMBER

1652

MAIL DATE

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PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Office Action Summary</b>	<b>Application No.</b> 10/590,705	<b>Applicant(s)</b> HASHIMOTO ET AL.	
	<b>Examiner</b> MD. YOUNUS MEAH	<b>Art Unit</b> 1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

#### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

- 1) ☒ Responsive to communication(s) filed on 08 July 2009.
- 2a) ☐ This action is **FINAL**.                      2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

- 4) ☒ Claim(s) 1-3 and 5-15 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-3 and 5-15 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All    b) ☐ Some \*    c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)                                | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                       | 5) <input type="checkbox"/> Notice of Informal Patent Application                       |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input type="checkbox"/> Other: _____  |

### **DETAILED ACTION**

Claims 1-3 and 5-15 were examined in the previous action.

Claims 1-3, 5-15 are currently pending in the instant application.

In response to a previous office action, (mailed on 04//01/2009), applicants on 07/08/2009 amended claims 7-14. Applicants' response on 07/08/2009 is acknowledged. Claims 1-3, 5-15 are under consideration.

Applicants' arguments filed on 07/08/2009 have been fully considered but they are found unpersuasive. Rejections and/or objections not reiterated from previous office actions are hereby withdrawn.

#### ***Claim Rejections 35 U.S.C. 1 12, second paragraph***

The following is a quotation of the second paragraph of 35 U.S.C. 112:  
The specification shall conclude with one or more claims particularly pointing out And distinctly claiming the subject matter, which the applicant regards as his invention.

Claims 1-3, 5-15 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 2-3, 5 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite in the recitation of "or a DNA which hybridizes ...with a DNA having....of the DNA" because it is unclear whether "the DNA" with whom "a DNA hybridizes" is the DNA encoding NADH dehydrogenase derived from the microorganisms referred in the claims or something else. Therefore examiner would interpret these claims openly and not limited to the specific plasmid/E. coli strain.

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Claims 6-7 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite in the recitation of “or a polypeptide comprising an amino acid sequence wherein 1 to 20 amino acid residues are deleted.....in the amino acid sequence of the polypeptide”. It is unclear whether “the polypeptide “ which is mutated by substitution of 1 to 20 amino acid residues, is the polypeptide having NADH dehydrogenase activity referred in the claims or something else. Examiner would interpret these claims openly and not limited to the specific plasmid/E. coli strain.

### **35 U.S.C 112 1st Paragraph**

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-3, 5-15 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1-3, 5-15 are directed to a method of production of amino acids by using a microorganism expressing a heterologous polynucleotide which is approximately 69.8% sequence identical to the polynucleotide of SEQ ID NO: 3 encoding a protein having NADH dehydrogenase activity or any heterologous DNA encoding NADH dehydrogenase wherein said DNA hybridizes to a DNA having any fragment which is

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complementary to SEQ ID NO: 3,5,7,9, 11, 13, or 15.

A calculation of the  $T_m$  of the polynucleotide recited in claim 1 shows that under the hybridization conditions recited, the recited polynucleotides can be approximately 69.8% sequence identical to the polynucleotide of SEQ ID NO: 3. Using the well known equation of Meinkoth and Wahl (Current Protocols in Molecular Biology, Hybridization Analysis of DNA Blots, pages 2.10.8-2.10.11, 1993),  $T_m = 81.5\text{ }^{\circ}\text{C} + 16.6 \times \log_{10}[\text{Na}^+] + 0.41 \times (\% \text{GC}) - .61 \times (\% \text{form}) - 500/L$ , the corresponding  $T_m$  for the polynucleotide recited is approximately  $95.2^{\circ}\text{C}$  assuming a G+C content of 50% and neglecting the term  $500/L$ , where  $L$  is the length in nucleotides of the probe ( $95.2\text{ }^{\circ}\text{C} = 81.5 + 16.6 \times \log_{10}[3.9 \times 2/20] + 0.41 \times (\%50) - .61(\% \text{form} = 0)$ ; for 2xSSC the molar concentration of  $\text{Na}^+$  is 3.9). As known in the art,  $T_m$  is reduced by approximately  $1\text{ }^{\circ}\text{C}$  for each 1% mismatching, therefore under the conditions recited (2xSSC and  $65\text{ }^{\circ}\text{C}$ ), a wash at  $65\text{ }^{\circ}\text{C}$  is equivalent to approximately 30.2% mismatching ( $30.2\% = 95.2^{\circ}\text{C} - 65^{\circ}\text{C}$ ). This level of mismatching amounts to 424 nucleotides which can be modified ( $424 = 0.302 \times 1404$ ) within SEQ ID NO: 3 (1404 nucleotides). Thus, the genus of polynucleotides recited encompass polynucleotides having at least 69.8% sequence identity with the polynucleotide of SEQ ID NO: 3. Since each of these nucleotide mismatches can affect a codon, the genus of polynucleotides recited can encompass polynucleotides where a great majority of the mismatches affects a codon, thus these polynucleotides can encompass polynucleotides having a protein having essentially no structural similarity with the polypeptide of SEQ ID NO: 4.

As discussed in the written description guidelines the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by actual reduction to practice, reduction to drawings, or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus. A representative number of species means that the species, which are adequately described, are representative of the entire genus. Thus, when there is substantial variation within the genus, one must describe a sufficient variety of species to reflect the variation within the genus. The specification teaches method of production of amino acid by using a microorganism expressing only a few heterologous DNA encoding NADH dehydrogenase of SEQ ID NO: 4, 6, 8, 10, 12, 14 or 16. Moreover, the specification fails to describe any other representative species by sufficient identifying characteristics or properties to show that applicant was in possession of the claimed genus.

There is no structure-function correlation with regard to the members of the genus of polypeptides having NADH dehydrogenase activity encoded by the polynucleotides recited in the instant claims. The specification discloses the structure of a few polynucleotides having the sequence of SEQ ID NO: 3,5,7,9, 11, 13, or 15 encoding the polypeptide having NADH dehydrogenase activity. No disclosure of the structural features required in any polynucleotide encoding the recited proteins has

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been provided. Nothing is known with regard to the structural elements that are essential and those that can be modified in the polynucleotide of SEQ ID NO: 3, 5, 7, 9, 11, 13, or 15 such that one could make a variant that encodes a protein having the desired activity. However the claimed method requires a genus of polynucleotides encoding a genus of polypeptides having essentially any structure (as for example any number of amino acid variations of SEQ ID NO: 4; encoded by polynucleotides having at least 69.8% sequence identity to the polynucleotide of SEQ ID NO: 3). This includes various allelic variants of the polypeptide of SEQ ID NO: 4 that the specification does not disclose. Therefore one of skill in the art would not recognize from the disclosure that applicants' were in possession of the claimed invention.

Applicants' are referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at [www.uspto.gov](http://www.uspto.gov).

Claims 1-3, 5-15 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a method of production of amino acids by using a microorganism expressing the heterologous DNAs of SEQ ID NOs: 3, 5, 7, 9, 11, 13 or 15 encoding the NADH dehydrogenases of SEQ ID NOs: 4, 6, 8, 10, 12, 14 or 16, does not reasonably provide enablement for a method of production of amino acids by using a microorganism expressing a heterologous polynucleotide which is approximately 69.8% sequence identical to the polynucleotide of SEQ ID NO: 3 encoding a protein having NADH dehydrogenase activity or any heterologous DNA encoding NADH

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dehydrogenase wherein said DNA hybridizes to a DNA having any fragment which is complementary to the polynucleotides of SEQ ID NO: 3,5,7,9, 11, 13, or 15. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims.

According to MPEP 2164.01(a), factors considered when determining whether there is sufficient evidence to support a determination that a disclosure does not satisfy the enablement requirement and whether any necessary experimentation is “undue” include, but are not limited to: (A) The breadth of the claims; (B) The nature of the invention; (C) The state of the prior art; (D) The level of one of ordinary skill; (E) The level of predictability in the art; (F) The amount of direction provided by the inventor; (G) The existence of working examples; and (H) The quantity of experimentation needed to make or use the invention based on the content of the disclosure.

MPEP§ 2164.04 states that while the analysis and conclusion of a lack of enablement are based on the factors discussed in MPEP § 2164.01(a) and the evidence as a whole, it is not necessary to discuss each factor in the written enablement rejection. The language should focus on those factors, reasons, and evidence that lead the examiner to conclude that the specification fails to teach how to make and use the claimed invention without undue experimentation, or that the scope of any enablement provided to one skilled in the art is not commensurate with the scope of protection sought by the claims. Accordingly, the factors most relevant to the instant rejection are addressed in detail below.



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Claims 1-3, 5-15 are so broad as to encompass a method of production of amino acids by using a microorganism expressing a heterologous polynucleotide which is approximately 69.8% sequence identical to the polynucleotide of SEQ ID NO: 3 encoding a protein having NADH dehydrogenase activity or any heterologous DNA encoding any NADH dehydrogenase wherein said DNA hybridizes to a DNA having any fragment which is complementary to SEQ ID NO: 3,5,7,9, 11, 13, or 15. The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polynucleotides of unknown structure encompassed by the claims. Since the amino acid sequence of a protein encoded by a given polynucleotide determines its structural and functional properties, predictability of which changes can be tolerated in the encoded protein's amino acid sequence to obtain the desired activity requires knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure relates to its function. However, in this case the disclosure is limited to a few polynucleotides comprising SEQ ID NOs: 3,5,7,9, 11, 13, or 15 encoding the polypeptides of SEQ ID NOs: 4, 6, 8, 10, 12, 14 or 16, respectively, wherein said encoded polypeptides have NADH dehydrogenase activity. It would require undue experimentation of the skilled artisan to make and use the claimed polynucleotides encoding said polypeptides. The specification is limited to the polynucleotides of SEQ ID NOs: 3,5,7,9, 11, 13, or 15 encoding the polypeptides of SEQ ID NOs: 4, 6, 8, 10, 12, 14 or 16 having NADH dehydrogenase activity but

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provides no guidance with regard to the making of variants and mutants or with regard to other uses. In view of the great breadth of the claims, amount of experimentation required to make the claimed polypeptides, the lack of guidance, working examples, and unpredictability of the art in predicting function from a polypeptide primary structure, the claimed invention would require undue experimentation. As such, the specification fails to teach one of ordinary skill how to make and/or use the polynucleotides encompassed by the claims.

While enzyme or polynucleotide isolation techniques, recombinant and mutagenesis techniques are known, and it is routine in the art to screen for multiple substitutions or multiple modifications as encompassed by the instant claims, the specific amino acid positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions.

The specification does not support the broad scope of the claims because the specification does not establish: (A) regions in the polynucleotide ( SEQ ID NO: 3,5,7,9, 11, 13, or 15) structure which may be modified without affecting its original activity of encoding a NADH dehydrogenase; (B) the general tolerance of NADH dehydrogenases to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any nucleotide with an expectation of obtaining a protein having the desired

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biological function; and (D) sufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including polynucleotides with an enormous number of nucleotide modifications to SEQ ID NO: 3,5,7,9, 11, 13, or 15. The scope of the claims must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of polynucleotides having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

### ***Claim Rejections 35 U.S.C 103a***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

Obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-3, 5-10, 14 and 15 remain rejected under 35 U.S.C. 103(a) by Bott *et al* (*J. Biotechnol*, 2003, 129-153, from IDS) in view of Molenaar *et al* (*J. Bacteriol*, 2000,

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6884-6891, from IDS), Hollander *et al* (*Appl Microbiol Biotechnol* 1994, 42, 508-515) and Nakagawa *et al* (US20020197605) for reasons of record. This rejection was discussed at length in the previous office action and discussed it again.

Bott *et al* describes the production of amino acids, such as, glutamate and L-lysine (page 130 left column, 1<sup>st</sup> pargh) by *Corynebacterium glutamicum* and that respiratory chain enzymes involved in the oxidative phosphorylation in the aerobic respiration of *Corynebacterium glutamicum* are useful in amino-acid production and one such enzyme is NADH dehydrogenase (abstract and FIG 1). However; Bott *et al* do not teach the method of producing amino acid by using microorganism transformed with heterologous NADH dehydrogenase derived from *Corynebacterium glutamicum*.

Molenaar *et al* teach NADH dehydrogenase gene of SEQ ID NO: 1 encoding NADH dehydrogenase (100% identical to applicants SEQ ID NO: 4) isolated from *Corynebacterium glutamicum* which is 100% identical to applicant NADH dehydrogenase gene of SEQ ID NO: 3 and Molenaar *et al* teach said NADH dehydrogenase is Type II NADH, wherein in the reaction number of proton discharged per electron is zero (page 6884, right column last paragraph). Molenaar *et al.* also teach that *Corynebacterium glutamicum* only expresses type II NADH dehydrogenase (page 6887, right column 1st paragraph).

Methods of expressing endogenous and exogenous genes in a host cell are well known in art to enhance the production of proteins and small organic compound. For example, Nakagawa *et al* teach an improved production of fine chemicals, such as, amino acid, and vitamins, by using a production strain of transformed host cell such as

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*E. coli* (subject matter of claims 8-9) with exogenous gene encoding desired enzymatic activities (page 7 paragraphs 0179-0191; page 14, paragraphs 0312-0313). Amino acids such as, L-lysine is industrially important chemicals.

It is well known in art that NADH is produced in several reactions in the amino acid biosynthesis pathway of *Corynebacterium glutamicum* (Hollander *et al. Appl Microbiol Biotechnol* 1994, 42, 508-515, Fig 1 at page 509). NADH dehydrogenase converts NADH to NAD. Hollander *et al* teach that quantitative yield of lysine can be produced from glucose in a fermentation system comprising *Corynebacterium*, if NADH and NADPH are consumed (its concentration is decreased) (last paragraph, page 514). Therefore, since type-II membrane bound NADH dehydrogenase of *Corynebacterium glutamicum* converts NADH to NAD, by doing so it depletes the NADH and increase the production of lysine from glucose. Although *E.coli* comprises two NADPH dehydrogenases (Type 1 and type II) they are different from that of NADH dehydrogenase (100% identical to applicants SEQ ID NO: 4) isolated from *Corynebacterium glutamicum* (only 27% sequence homology, page 132, Bott *et al.*). Therefore, in order to produce amino acid in large scale, one of ordinary skill in the art is **motivated** to express *E.coli* (as taught Nakagawa *et al*) with NADH dehydrogenase gene of SEQ ID NO: 1 of *Corynebacterium glutamicum* of Molenaar *et al* and use the said transformed microorganism in the method of production of amino acid.

As such it would have been obvious to one of ordinary skill in the art to use Molenaar *et al* NADH gene of SEQ ID NO: 1 encoding a type II NADH dehydrogenase (which discharge zero proton per electron) isolated from *Corynebacterium glutamicum*

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which is 100% identical to applicant NADH gene of SEQ ID NO: 3 express the said gene in *E. coli* and use the transformed *E. coli* to the method of production of amino acid.

Claims 5 and 7 are included in the above rejection because; although these claims are directed to specific plasmid/*E. coli* strain; however, as explain in the 112 2<sup>nd</sup> paragraph rejection these claims are interpreted openly and not limited to the specific plasmid/*E. coli* strain.

Claims 11-13 are rejected under 35 U.S.C. 103(a) by Bott *et al* (*J. Biotechnol*, 2003, 129-153, from IDS) in view of Molenaar *et al* (*J. Bacteriol*, 2000, 6884-6891), Hollander *et al* (*Appl Microbiol. Biotechnol.* 1994, 42, 508-515) and Nakagawa *et al* (US20020197605).

The teaching of Bott *et al*, Hollander *et al* and Nakagawa *et al* is discussed above for the 35 U.S.C. 103(a) rejection of claims 1-3, 6, 8-9, 14-15. However Bott *et al*, Hollander *et al* and Nakagawa *et al* do not teach explicitly a process of producing amino acids using *Corynebacterium glutamicum* expressing heterologous NADH-II dehydrogenase gene of SEQ ID NO: 1.

Since Bott *et al* describes the production of amino acids by *Corynebacterium glutamicum* in the biosynthesis of amino acids use different respiratory chain enzymes and one of the enzymes used is NADH dehydrogenase (NADH-II), in order to further enhance the production of amino acids by *Corynebacterium*, one ordinary skill in the art is motivated to express heterologous NADH-II dehydrogenase gene of SEQ ID NO: 1 of

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Molenaar *et al.*) in *Corynebacterium* or *Corynebacterium glutamicum*. One of ordinary skill in the art would reasonably expect this to increase the amount of the NADH-II dehydrogenase produced in the *Corynebacterium* and therefore, enhance the amino acid production.

As such it would have been obvious to one of ordinary skill in the art to use Molenaar *et al* NADH dehydrogenase gene of SEQ ID NO: 1 encoding type II NADH dehydrogenase isolated from *Corynebacterium glutamicum* which is 100% identical to applicant NADH gene of SEQ ID NO: 3 express the said gene in *corynebacterium* or *Corynebacterium glutamicum* and use the transformed *Corynebacterium* or *Corynebacterium glutamicum* to the method of production of amino acid, as taught by Bott *et al.*

### ***Arguments and response***

Applicants argue, at pages 8-9 of their amendment of 07/08/2009, that *Corynebacterium glutamicum* contains only NADH-II gene as only membrane bound NADH dehydrogenase gene and further refer to another prior art Nakai *et al* (US2002/0160461) showing that mutation of energy non-producing NADH-II in *E. coli* does not effect the amino acid production in *E. coli*. Applicants' further argue that *Corynebacterium glutamicum* probably uses other dehydrogenases that consume NADH/NADPH in the production of amino acid. Applicants' also argue that one of ordinary skill in the art would not introduce NADH dehydrogenase gene ( encodes NADH-II dehydrogenase) to *Corynebacterium glutamicum* (as taught by Molenaar et

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al) which is 100% identical to applicant NADH gene of SEQ ID NO: 3 to a microorganism for the production of amino acids.

Applicants' arguments filed on 07/08/2009 have been fully considered, but they found unpersuasive. Although *E.coli* comprises two NADPH dehydrogenases (Type I and type II) they are different from that of NADH II dehydrogenase (100% identical to applicants SEQ ID NO: 4) isolated from *Corynebacterium glutamicum* (only 27% sequence homology to *E.coli* NADH-II, page 132, Bott et al.). As discussed above *Corynebacterium glutamicum* is an amino acid producing microorganism having only a type II NADH dehydrogenase. Said NADH dehydrogenase involved as a primary dehydrogenase, linked with central metabolism, in the respiratory chain of *Corynebacterium glutamicum* and its growth and for the production of amino acids. One of ordinary skill in the art would recognize that NADH-II dehydrogenase of *Corynebacterium glutamicum* is involved in amino acid production in *Corynebacterium glutamicum*. With regard to the teachings of Nakai et al (US2002/0160461), it is noted that (1) NADH-II dehydrogenase (100% identical to applicants SEQ ID NO: 4) isolated from *Corynebacterium glutamicum* (only 27% sequence homology to that of *E. coli*) is not the same NADH-II of *E. coli*; and (2) Nakai et al teach that (Table 2, page 20) over-expression of cytochrome bo-type oxidoreductase (CYO) in *E.coli* increases the amino acid production. Production of lysine in transformed *E.coli* strain increases from .29g/L (wild-type) to .48-.53 g/L (over-expressed CYO). NADH-I is involved in cytochrome bo-type oxidoreductase pathway, not NADH-II (pages 1-2, Nakai et al). In Nakai et al's, *E. coli* strain over-expressed with cytochrome bo-type oxidoreductase



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(CYO) uses NADH I dehydrogenase in the amino acid production, not the NADH-II. Therefore; mutation of NADH-II in the said *E. coli* strain does shows little effect on amino acid production. The CYO over-expressed *E.coli* strain produces 0.48 g/L of lysine when NADH-II of said strain is not mutated and produces 0.53 g/L of lysine when NADH-II is mutated (within experimental error 0.48 and 0.53 are same, Table 2, page 20). Applicants' argument that *Corynebacterium glutamicum* probably uses other dehydrogenases that consume NADH/NADPH in the production of amino acid is considered. However, as explained above since *Corynebacterium glutamicum* uses type-II NADH dehydrogenase in the central metabolism, in the respiratory chain, growth and amino acid biosynthesis, one ordinary skill in the art would introduce Molenaar *et al* NADH gene of SEQ ID NO: 1 isolated from *Corynebacterium glutamicum* which is 100% identical to applicant NADH gene of SEQ ID NO: 3 to a microorganism to enhance the production of amino acid. Moreover as explained above NADH dehydrogenase converts NADH to NAD. Hollander *et al* teach that quantitative yield of lysine can be produced from glucose in a fermentation system comprising *Corynebacterium*, if NADH and NADPH are consumed (its concentration is decreased) (last paragraph, page 514). Therefore, since type-II membrane bound NADH dehydrogenase of *Corynebacterium glutamicum* converts NADH to NAD, by doing so it depletes the NADH and increase the production of lysine from glucose. Therefore, in order to produce amino acid in large scale, one of ordinary skill in the art is **motivated** to express *E.coli* (as taught Nakagawa *et al*) with NADH dehydrogenase gene of SEQ ID NO: 1 (encoding Type-II membrane bound NADH dehydrogenase) of *Corynebacterium glutamicum* of Molenaar

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*et al* and use the said transformed microorganism in the method of production of amino acid.]Thus, the claimed invention remains *prima facie* obvious over the prior art of record.

***Allowable Subject Matter/Conclusion***

None of the claims are allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Mohammad Meah whose telephone number is 571-272-1261. The examiner can normally be reached on 8:30-5PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Andrew Wang can be reached on 571-272-0811. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Mohammad Younus Meah  
Examiner, Art Unit 1652

/Delia M. Ramirez/  
Primary Examiner, Art Unit 1652